



US 70
0824

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/931,009

Source: OIP

Date Processed by STIC: 8/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 08/27/2001

PATENT APPLICATION: US/09/931,009

TIME: 12:32:12

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\08272001\I931009.raw

5 <110> APPLICANT: Smith, Theresa H.
W--> 6 <120> TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
W--> 7 <130> FILE REFERENCE: US 1257/01 (VA)
W--> 8 <140> CURRENT APPLICATION NUMBER:
C--> 9 <141> CURRENT FILING DATE: 2001-08-17
W--> 9 <150> PRIOR APPLICATION NUMBER:
W--> 10 <151> PRIOR FILING DATE:
W--> 11 <160> NUMBER OF SEQ ID: 2

ERRORED SEQUENCES

W--> 12 <210> SEQ ID NO: 1
13 <211> LENGTH: 620
14 <212> TYPE: PRT
W--> 15 <213> ORGANISM:
W--> 16 <220> FEATURE:
W--> 17 <221> NAME/KEY:
18 <222> LOCATION:
19 <223> OTHER INFORMATION: STRANDEDNESS: single
20 TOPOLOGY: both
E--> 23 <400> SEQUENCE: 0
24 Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly Gly Val
25 5 10 15
27 Arg Gly Pro Arg Val Val Glu Arg His Gln Ser Ala Cys Lys Asp
28 20 25 30
30 Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys
31 35 40 45
33 Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn Gln
34 50 55 60
36 Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu
37 65 70 75
39 Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile
40 80 85 90
42 Met Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp
43 95 100 105
45 Asn Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu
46 110 115 120
48 Val Leu Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu
49 125 130 135
51 Leu Gln Lys Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu
52 140 145 150
54 Glu Val Asp Ile Asp Ile Lys Ile Arg Ser Cys Arg Gly Ser Cys
55 155 160 165
57 Ser Arg Ala Leu Ala Arg Glu Val Asp Leu Lys Asp Tyr Glu Asp
58 170 175 180
60 Gln Gln Lys Gln Leu Glu Gln Val Ile Ala Lys Asp Leu Leu Pro

Does Not Comply
Corrected Diskette Needed

*All following pages
for explanation*

*Please
consult
Sequence Rules
for valid
format*

09/93/009 2

SEQUENCE LISTING

<110> Smith, Theresa H.
 <120> PRO-INFLAMMATORY FIBRINOPEPTIDE
 <130> US 1257/01 (VA)
 <140>
 <150>
 <151>
 <160> 2
 <210> 1
 <211> 620
 <212> PRT
 <213> *mandatory response needed*
 <220>
 <221>
 <222>
 <223> ~~STRANDEDNESS: single~~
 ~~TOPOLOGY: both~~

*see item 11 on Enon
 summary sheet*

*not used in new sequence rules
 format*

delete
 <400> ~~SEQ ID NO: 1~~
 Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly Gly Val
 5 10 15
 Arg Gly Pro Arg Val Val Glu Arg His Gln Ser Ala Cys Lys Asp
 20 25 30
 Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys
 35 40 45
 Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn Gln
 50 55 60
 Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu
 65 70 75
 Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile
 80 85 90
 Met Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp
 95 100 105
 Asn Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu
 110 115 120
 Val Leu Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu
 125 130 135
 Leu Gln Lys Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu
 140 145 150
 Glu Val Asp Ile Asp Ile Lys Ile Arg Ser Cys Arg Gly Ser Cys
 155 160 165
 Ser Arg Ala Leu Ala Arg Glu Val Asp Leu Lys Asp Tyr Glu Asp

170	175	180
Gln Gln Lys Gln Leu Glu Gln Val Ile	Ala Lys Asp Leu Leu Pro	
185	190	195
Ser Arg Asp Arg Gln His Leu Pro Leu	Ile Lys Met Lys Pro Val	
200	205	210
Pro Asp Leu Val Pro Gly Asn Phe Lys	Ser Gln Leu Gln Lys Val	
215	220	225
Pro Pro Glu Trp Lys Ala Leu Thr Asp	Met Pro Gln Met Arg Met	
230	235	240
Glu Leu Glu Arg Pro Gly Gly Asn Glu	Ile Thr Arg Gly Gly Ser	
245	250	255
Thr Ser Tyr Gly Thr Gly Ser Glu Thr	Glu Ser Pro Arg Asn Pro	
260	265	270
Ser Ser Ala Gly Ser Trp Asn Ser Gly	Ser Ser Gly Pro Gly Ser	
275	280	285
Thr Gly Asn Arg Asn Pro Gly Ser Ser	Gly Thr Gly Gly Thr Ala	
290	295	300
Thr Trp Lys Pro Gly Ser Ser Gly Pro	Gly Ser Thr Gly Ser Trp	
305	310	315
Asn Ser Gly Ser Ser Gly Thr Gly Ser	Thr Gly Asn Gln Asn Pro	
320	325	330
Gly Ser Pro Arg Pro Gly Ser Thr Gly	Thr Trp Asn Pro Gly Ser	
335	340	345
Ser Glu Arg Gly Ser Ala Gly His Trp	Thr Ser Glu Ser Ser Val	
350	355	360
Ser Gly Ser Thr Gly Gln Trp His Ser	Glu Ser Gly Ser Phe Arg	
365	370	375
Pro Asp Ser Pro Gly Ser Gly Asn Ala	Arg Pro Asn Asn Pro Asp	
380	385	390
Trp Gly Thr Phe Glu Glu Val Ser Gly	Asn Val Ser Pro Gly Thr	
395	400	405
Arg Arg Glu Tyr His Thr Glu Lys Leu	Val Thr Ser Lys Gly Asp	
410	415	420
Lys Glu Leu Arg Thr Gly Lys Glu Lys	Val Thr Ser Gly Ser Thr	
425	430	435
Thr Thr Thr Arg Arg Ser Cys Ser Lys	Thr Val Thr Lys Thr Val	
440	445	450
Ile Gly Pro Asp Gly His Lys Glu Val	Thr Lys Glu Val Val Thr	

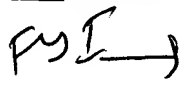
455	460	465
Ser Glu Asp Gly Ser Asp Cys Pro Glu	Ala Met Asp Leu Gly Thr	
470	475	480
Leu Ser Gly Ile Gly Thr Leu Asp Gly	Phe Arg His Arg His Pro	
485	490	495
Asp Glu Ala Ala Phe Phe Asp Thr Ala	Ser Thr Gly Lys Thr Phe	
500	505	510
Pro Gly Phe Phe Ser Pro Met Leu Gly	Glu Phe Val Ser Glu Thr	
515	520	525
Glu Ser Arg Gly Ser Glu Ser Gly Ile	Phe Thr Asn Thr Lys Glu	
530	535	540
Ser Ser Ser His His Pro Gly Ile Ala	Glu Phe Pro Ser Arg Gly	
545	550	555
Lys Ser Ser Ser Tyr Ser Lys Gln Phe	Thr Ser Ser Thr Ser Tyr	
560	565	570
Asn Arg Gly Asp Ser Thr Phe Glu Ser	Lys Ser Tyr Lys Met Ala	
575	580	585
Asp Glu Ala Gly Ser Glu Ala Asp His	Glu Gly Thr His Ser Thr	
590	595	600
Lys Arg Gly His Ala Lys Ser Arg Pro	Val Arg Gly Ile His Thr	
605	610	615
Ser Pho Leu Gly Lys		
620		

<210> 2
 <211> 4
 <212> PRT
 <213> Artificial Sequence
 <220>
 <221>
 <222>
 <223> DESCRIPTION OF ARTIFICIAL SEQUENCE: peptide
 STRANDEDNESS: single
 TOPOLOGY: linear
 <400> SEQ ID NO: 2
 Gly Pro Arg Pro

*insufficient explanation
 for Artificial Sequence,
 give source of
 genetic material
 (see item 11 on
 Error Summary
 sheet)*

delete

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/931,009
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220> 	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	